RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/562,778_

Source: _1 Fwo_

Date Processed by STIC: _8/24/06_

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RAW SEQUENCE LISTING   DATE: 08/24/2006
PATENT APPLICATION: US/10/562,778   TIME: 15:01:14

Input Set : **A:\Sequence Listing.ST25.txt**
Output Set: **N:\CRF4\08242006\J562778.raw**

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 3 <110> APPLICANT: Chai, Zhonglin
 4        Cooper, Mark Emmanuel
 5        Cao, Zemin
 7 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING DISORDERS OF THE
 8        EXTRACELLULAR MATRIX
10 <130> FILE REFERENCE: 002354/000370
12 <140> CURRENT APPLICATION NUMBER: 10/562,778
13 <141> CURRENT FILING DATE: 2005-12-29
15 <150> PRIOR APPLICATION NUMBER: AU2003903363
16 <151> PRIOR FILING DATE: 2003-07-01
18 <150> PRIOR APPLICATION NUMBER: PCT/AU2004/000873
19 <151> PRIOR FILING DATE: 2004-06-30
21 <160> NUMBER OF SEQ ID NOS: 2
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 2867
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
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35 cggtcgccat ggaccgccca gatgaggggc ctccggccaa gacccgccgc ctgagcagct     180
37 ccgagtctcc acagcgcgac ccgccccccgc cgccgccgcc gccgccgctc ctccgactgc     240
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47 tcccccactcc tgaggcctcg ggggggagcc tggaaatcga ttttcaggtt gtacagtcga     540
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53 atgagcggga gagtatgagg agcagcagga ggcggcggcg gcggcggagg aggaagcaga     720
55 ggaaggtgaa gagggaaagc agagagagaa atgccgagag gatggagagc atcctgcagg     780
57 cactggagga tattcagctg gatctggagg cagtgaacat caaggcaggc aaagccttcc     840
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63 ttttgatcaa ccgacgtgat gaagacattt tccgctactt gaccaatctg caggtacagg    1020
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71 aggatgcgag ccacagcttt ttcagctggt tctcaaacca tagcctccca gaggctgaca    1260
73 ggattgctga gattatcaag aatgatctgt gggttaaccc tctacgctac tacctgagag    1320
75 aaaggggctc caggataaag agaaagaagc aagaaatgaa gaaacgtaaa accaggggca    1380
77 gatgtgaggt ggtgatcatg gaagacgccc ctgactatta tgcagtggaa gacatttttca   1440
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 83 acagcgagaa tcctgaccac aatgaggtcc ccaacaacga gaccactgat aacaacgaga   1620
 85 gcgctgatga ccacgaaacc actgacaaca atgagagtgc agatgacaac aacgagaatc   1680
 87 ctgaagacaa taacaagaac actgatgaca acgaagagaa ccctaacaac aacgagaaca   1740
 89 cttacggcaa caacttcttc aaaggtggct ctggggcag. ccatggcaac aaccaggaca   1800
 91 gcagcgacag tgacaatgaa gcagatgagg ccagtgatga tgaagataat gatggcaacg   1860
 93 aaggtgacaa tgagggcagt gatgatgatg gcaatgaagg tgacaatgaa ggcagcgatg   1920
 95 atgacgacag agacattgag tactatgaga aagttattga agactttgac aaggatcagg   1980
 97 ctgactacga ggacgtgata gagatcatct cagacgaatc agtggaagaa gagggcattg   2040
 99 aggaaggcat ccagcaagat gaggacatct atgaggaagg aaactatgag gaggaaggaa   2100
101 gtgaagatgt ctgggaagaa ggggaagatt cggacgactc tgacctagag gatgtgcttc   2160
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111 ctagtcccct tcttttggcc ctccgccccc gcaggcttct gtgtgctgct aactgtattt   2460
113 attgtgatgc cttggtcagg gcccctctac ccacttctcc cagtcagttg tggccccagc   2520
115 ccctctccct gtgctgtgtg gagtggacac cctgacccce gaagcgggga gggccgctgt   2580
117 ggccttcgtc acagccgcgc agtgcccatg gaggcgctgc tgccaccttc ctctcccaag   2640
119 ttctttctcc atccctctcc tcttcccgcc gcgccgctag cccgcctcgg tgtctatgca   2700
121 aggccgcttc gccattgcgg tattctttgc ggtattcttg tccccgtccc ccagaaggct   2760
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128 <210> SEQ ID NO: 2
129 <211> LENGTH: 693
130 <212> TYPE: PRT
131 <213> ORGANISM: Homo sapiens
133 <400> SEQUENCE: 2
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139 Ser Ser Glu Ser Pro Gln Arg Asp Pro Pro Pro Pro Pro Pro Pro Pro
140             20                  25                  30
143 Pro Leu Leu Arg Leu Pro Leu Pro Pro Gln Gln Arg Pro Arg Leu
144         35                  40                  45
147 Gln Glu Glu Thr Glu Ala Ala Gln Val Leu Ala Asp Met Arg Gly Val
148     50                  55                  60
151 Gly Leu Gly Pro Ala Leu Pro Pro Pro Pro Tyr Val Ile Leu Glu
152 65                  70                  75                  80
155 Glu Gly Gly Ile Arg Ala Tyr Phe Thr Leu Gly Ala Glu Cys Pro Gly
156                 85                  90                  95
159 Trp Asp Ser Thr Ile Glu Ser Gly Tyr Gly Glu Ala Pro Pro Pro Thr
160                 100                 105                 110
163 Glu Ser Leu Glu Ala Leu Pro Thr Pro Glu Ala Ser Gly Gly Ser Leu
164             115                 120                 125
167 Glu Ile Asp Phe Gln Val Val Gln Ser Ser Ser Phe Gly Gly Glu Gly
168     130                 135                 140
171 Ala Leu Glu Thr Cys Ser Ala Val Gly Trp Ala Pro Gln Arg Leu Val
172 145                 150                 155                 160
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176             165             170             175
179 Glu Asp Glu Arg Glu Ser Met Arg Ser Ser Arg Arg Arg Arg Arg Arg
180             180             185             190
183 Arg Arg Arg Lys Gln Arg Lys Val Lys Arg Glu Ser Arg Glu Arg Asn
184         195             200             205
187 Ala Glu Arg Met Glu Ser Ile Leu Gln Ala Leu Glu Asp Ile Gln Leu
188     210             215             220
191 Asp Leu Glu Ala Val Asn Ile Lys Ala Gly Lys Ala Phe Leu Arg Leu
192 225             230             235             240
195 Lys Arg Lys Phe Ile Gln Met Arg Arg Pro Phe Leu Glu Arg Arg Asp
196             245             250             255
199 Leu Ile Ile Gln His Ile Pro Gly Phe Trp Val Lys Ala Phe Leu Asn
200             260             265             270
203 His Pro Arg Ile Ser Ile Leu Ile Asn Arg Arg Asp Glu Asp Ile Phe
204         275             280             285
207 Arg Tyr Leu Thr Asn Leu Gln Val Gln Asp Leu Arg His Ile Ser Met
208     290             295             300
211 Gly Tyr Lys Met Lys Leu Tyr Phe Gln Thr Asn Pro Tyr Phe Thr Asn
212 305             310             315             320
215 Met Val Ile Val Lys Glu Phe Gln Arg Asn Arg Ser Gly Arg Leu Val
216         .       325             330             335
219 Ser His Ser Thr Pro Ile Arg Trp His Arg Gly Gln Glu Pro Gln Ala
220             340             345             350
223 Arg Arg His Gly Asn Gln Asp Ala Ser His Ser Phe Phe Ser Trp Phe
224         355             360             365
227 Ser Asn His Ser Leu Pro Glu Ala Asp Arg Ile Ala Glu Ile Ile Lys
228     370             375             380
231 Asn Asp Leu Trp Val Asn Pro Leu Arg Tyr Tyr Leu Arg Glu Arg Gly
232 385             390             395             400
235 Ser Arg Ile Lys Arg Lys Lys Gln Glu Met Lys Lys Arg Lys Thr Arg
236             405             410             415
239 Gly Arg Cys Glu Val Val Ile Met Glu Asp Ala Pro Asp Tyr Tyr Ala
240         420             425             430
243 Val Glu Asp Ile Phe Ser Glu Ile Ser Asp Ile Asp Glu Thr Ile His
244         435             440             445
247 Asp Ile Lys Ile Ser Asp Phe Met Glu Thr Thr Asp Tyr Phe Glu Thr
248     450             455             460
251 Thr Asp Asn Glu Ile Thr Asp Ile Asn Glu Asn Ile Cys Asp Ser Glu
252 465             470             475             480
255 Asn Pro Asp His Asn Glu Val Pro Asn Asn Glu Thr Thr Asp Asn Asn
256             485             490             495
259 Glu Ser Ala Asp Asp His Glu Thr Thr Asp Asn Asn Glu Ser Ala Asp
260             500             505             510
263 Asp Asn Asn Glu Asn Pro Glu Asp Asn Asn Lys Asn Thr Asp Asp Asn
264         515             520             525
267 Glu Glu Asn Pro Asn Asn Asn Glu Asn Thr Tyr Gly Asn Asn Phe Phe
268     530             535             540
271 Lys Gly Gly Phe Trp Gly Ser His Gly Asn Asn Gln Asp Ser Ser Asp
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272 545                   550                   555                   560
275 Ser Asp Asn Glu Ala Asp Glu Ala Ser Asp Asp Glu Asp Asn Asp Gly
276             565                   570                   575
279 Asn Glu Gly Asp Asn Glu Gly Ser Asp Asp Asp Gly Asn Glu Gly Asp
280             580                   585                   590
283 Asn Glu Gly Ser Asp Asp Asp Asp Arg Asp Ile Glu Tyr Tyr Glu Lys
284         595                   600                   605
287 Val Ile Glu Asp Phe Asp Lys Asp Gln Ala Asp Tyr Glu Asp Val Ile
288     610                   615                   620
291 Glu Ile Ile Ser Asp Glu Ser Val Glu Glu Glu Gly Ile Glu Glu Gly
292 625                   630                   635                   640
295 Ile Gln Gln Asp Glu Asp Ile Tyr Glu Glu Gly Asn Tyr Glu Glu Glu
296             645                   650                   655
299 Gly Ser Glu Asp Val Trp Glu Glu Gly Glu Asp Ser Asp Asp Ser Asp
300             660                   665                   670
303 Leu Glu Asp Val Leu Gln Val Pro Asn Gly Trp Ala Asn Pro Gly Lys
304         675                   680                   685
307 Arg Gly Lys Thr Gly
308     690
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VERIFICATION SUMMARY   DATE: 08/24/2006
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